PCT09

RAW SEQUENCE LISTING   DATE: 10/26/2001
PATENT APPLICATION: US/09/744,125   TIME: 15:05:43

Input Set : A:\st98045sqlt.txt
Output Set: N:\CRF3\10262001\I744125.raw

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 3 <110> APPLICANT: MARCIREAU, Christophe
 4        MULTON, Marie-Christine
 5        POLARD-HOUSET, Valerie
 7 <120> TITLE OF INVENTION: MEKK1-INTERACTING FHA PROTEIN (M1F1)
 9 <130> FILE REFERENCE: A3233A US
11 <140> CURRENT APPLICATION NUMBER: 09/744,125
12 <141> CURRENT FILING DATE: 2001-01-19
14 <150> PRIOR APPLICATION NUMBER: PCT/EP99/05142
15 <151> PRIOR FILING DATE: 1999-07-21
17 <150> PRIOR APPLICATION NUMBER: US 60/093,590
18 <151> PRIOR FILING DATE: 1998-07-21
20 <160> NUMBER OF SEQ ID NOS: 15
22 <170> SOFTWARE: PatentIn version 3.0
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25 <211> LENGTH: 2973
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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40 ccagagaatt ttgtagacat caagaaaact ttggaacgag agactcgcca gtgccaggct    360
42 ctggtgatct ggactgactg tgatagagaa ggcgaaaaca tcgggtttga gattatccac    420
44 gtgtgtaagg ctgtaaagcc caatctgcag gtgttgcgag cccgattctc tgagatcaca    480
46 ccccatgccg tcaggacagc ttgtgaaaac ctgaccgagc ctgatcagag ggtgagcgat    540
48 gctgtggatg tgaggcagga gctggacctg aggattggag ctgcctttac taggttccag    600
50 accctgcggc ttcagaggat ttttcctgag gtgctggcag agcagctcat cagttacggc    660
52 agctgccagt tccccacact gggctttgtg gtggagcggt tcaaagccat tcaggctttt    720
54 gtaccagaaa tcttccacag aattaaagta actcatgacc acaaagatgg tatcgtagaa    780
56 ttcaactgga aaaggcatcg actctttaac cacacggctt gcctagttct ctatcagttg    840
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60 cggcctcaag ccttggacac tgtggagctt gagaagctgg cttctcgaaa gttgagaata    960
62 aatgctaaag aaaccatgag gattgctgag aagctctaca ctcaagggta catcagctat   1020
64 ccccgaacag aaacaaacat ttttcccaga gacttaaacc tgacggtgtt ggtggaacag   1080
66 cagacccccg atccacgctg ggggggcctt gcccagagca ttctagagcg gggtggtccc   1140
68 accccacgca atgggaacaa gtctgaccaa gctcaccctc ccattcaccc caccaaatac   1200
70 accaacaact tacagggaga tgaacagcga ctgtacgagt ttattgttcg ccatttcctg   1260
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74 gaacgctttg tggcccatgg cctcatgatt ctggcccgaa actatctgga tgtgtatcca   1380
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80 ctcattgccc tcatggagaa gcatggcatt ggtacggatg ccactcatgc ggagcacatc   1560
82 gagaccatca agcccggat gtacgtgggc ctcaccccag acaagcggtt cctccctggg   1620
84 cacctgggca tgggacttgt ggaaggttat gattccatgg gctatgaaat gtctaagcct   1680
86 gacctccggg ctgaactgga agctgatctg aagctgatct gtgatggcaa aaaggacaaa   1740
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 90 aaagcaaaga aattggacga ggccttggcc cagtactttg ggaatgggac agagttggcc  1860
 92 cagcaagaag atatctaccc agccatgcca gagcccatca ggaagtgccc acagtgcaac  1920
 94 aaggacatgg tccttaagac caagaagaat ggcgggttct acctcagctg catgggtttc  1980
 96 ccagagtgtc gctcagctgt gtggcttcct gactcggtgc tggaggccag cagggacagc  2040
 98 agtgtgtgtc cagtttgtca gccacaccct gtgtacaggt taaagttaaa gtttaagcgc  2100
100 ggtagccttc ccccgaccat gcctctggag tttgtttgct gcatcggcgg atgcgacgac  2160
102 accctgaggg agatcctgga cctgagattt tcaggggcc cccccagggc tagccagccc  2220
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106 cctgctgaca gcagacagac tgggtcctca aaggctctgg cccagaccct cccaccaccc  2340
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110 actgtccgta aggagggccc caaccggggc cggcagttct ttaagtgcaa cggaggtagc  2460
112 tgcaacttct tcctgtgggc agacagcccc aatccgggag caggagggcc tcctgccttg  2520
114 gcatatagac ccctgggcgc ctccctggga tgcccaccag gcccagggat ccacctaggt  2580
116 gggtttggca accctggtga tggcagtggt agtggcacat cctgcctttg cagccagccc  2640
118 tccgtcacac ggactgtgca gaaggatgga cccaacaagg ggcgccagtt ccacacatgt  2700
120 gccaagccga gagagcagca gtgtggcttt ttccagtggg tcgatgagaa caccgctcca  2760
122 gggacttctg gagccccgtc ctggacagga gacagaggaa gaaccctgga gtcggaagcc  2820
124 agaagcaaaa ggccccgggc cagttcctca gacatggggt ccacagcaaa gaaacccggg  2880
126 aaatgcagcc tttgccacca gcctggacac acccgtccct tttgtcctca gaacagatga  2940
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144 Arg Arg Glu Gly Leu Ser Lys Phe Asn Lys Ile Tyr Glu Phe Asp Tyr
145         35                  40                  45
147 His Leu Tyr Gly Gln Asn Val Thr Met Val Met Thr Ser Val Ser Gly
148     50                  55                  60
150 His Leu Leu Ala His Asp Phe Gln Met Gln Phe Arg Lys Trp Gln Ser
151 65                  70                  75                  80
153 Cys Asn Pro Leu Val Leu Phe Glu Ala Glu Ile Glu Lys Tyr Cys Pro
154             85                  90                  95
156 Glu Asn Phe Val Asp Ile Lys Lys Thr Leu Glu Arg Glu Thr Arg Gln
157             100                 105                 110
159 Cys Gln Ala Leu Val Ile Trp Thr Asp Cys Asp Arg Glu Gly Glu Asn
160         115                 120                 125
162 Ile Gly Phe Glu Ile Ile His Val Cys Lys Ala Val Lys Pro Asn Leu
163     130                 135                 140
165 Gln Val Leu Arg Ala Arg Phe Ser Glu Ile Thr Pro His Ala Val Arg
166 145                 150                 155                 160
168 Thr Ala Cys Glu Asn Leu Thr Glu Pro Asp Gln Arg Val Ser Asp Ala
169             165                 170                 175
171 Val Asp Val Arg Gln Glu Leu Asp Leu Arg Ile Gly Ala Ala Phe Thr
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174 Arg Phe Gln Thr Leu Arg Leu Gln Arg Ile Phe Pro Glu Val Leu Ala
175         195              200              205
177 Glu Gln Leu Ile Ser Tyr Gly Ser Cys Gln Phe Pro Thr Leu Gly Phe
178     210              215              220
180 Val Val Glu Arg Phe Lys Ala Ile Gln Ala Phe Val Pro Glu Ile Phe
181 225             230              235              240
183 His Arg Ile Lys Val Thr His Asp His Lys Asp Gly Ile Val Glu Phe
184             245              250              255
186 Asn Trp Lys Arg His Arg Leu Phe Asn His Thr Ala Cys Leu Val Leu
187         260              265              270
189 Tyr Gln Leu Cys Val Glu Asp Pro Met Ala Thr Val Val Glu Val Arg
190     275              280              285
192 Ser Lys Pro Lys Ser Lys Trp Arg Pro Gln Ala Leu Asp Thr Val Glu
193     290              295              300
195 Leu Glu Lys Leu Ala Ser Arg Lys Leu Arg Ile Asn Ala Lys Glu Thr
196 305             310              315              320
198 Met Arg Ile Ala Glu Lys Leu Tyr Thr Gln Gly Tyr Ile Ser Tyr Pro
199             325              330              335
201 Arg Thr Glu Thr Asn Ile Phe Pro Arg Asp Leu Asn Leu Thr Val Leu
202     340              345              350
204 Val Glu Gln Gln Thr Pro Asp Pro Arg Trp Gly Ala Phe Ala Gln Ser
205     355              360              365
207 Ile Leu Glu Arg Gly Gly Pro Thr Pro Arg Asn Gly Asn Lys Ser Asp
208     370              375              380
210 Gln Ala His Pro Pro Ile His Pro Thr Lys Tyr Thr Asn Asn Leu Gln
211 385             390              395              400
213 Gly Asp Glu Gln Arg Leu Tyr Glu Phe Ile Val Arg His Phe Leu Ala
214             405              410              415
216 Cys Cys Ser Gln Asp Ala Gln Gly Gln Glu Thr Thr Val Glu Ile Asp
217     420              425              430
219 Ile Ala Gln Glu Arg Phe Val Ala His Gly Leu Met Ile Leu Ala Arg
220     435              440              445
222 Asn Tyr Leu Asp Val Tyr Pro Tyr Asp His Trp Ser Asp Lys Ile Leu
223     450              455              460
225 Pro Val Tyr Glu Gln Gly Ser His Phe Gln Pro Ser Thr Val Glu Met
226 465             470              475              480
228 Val Asp Gly Glu Thr Ser Pro Pro Lys Leu Leu Thr Glu Ala Asp Leu
229             485              490              495
231 Ile Ala Leu Met Glu Lys His Gly Ile Gly Thr Asp Ala Thr His Ala
232         500              505              510
234 Glu His Ile Glu Thr Ile Lys Ala Arg Met Tyr Val Gly Leu Thr Pro
235     515              520              525
237 Asp Lys Arg Phe Leu Pro Gly His Leu Gly Met Gly Leu Val Glu Gly
238     530              535              540
240 Tyr Asp Ser Met Gly Tyr Glu Met Ser Lys Pro Asp Leu Arg Ala Glu
241 545             550              555              560
243 Leu Glu Ala Asp Leu Lys Leu Ile Cys Asp Gly Lys Lys Asp Lys Phe
244             565              570              575
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246 Val Val Leu Arg Gln Gln Val Gln Lys Tyr Lys Gln Val Phe Ile Glu
247       .     580           585           590
249 Ala Val Ala Lys Ala Lys Lys Leu Asp Glu Ala Leu Ala Gln Tyr Phe
250         595           600           605
252 Gly Asn Gly Thr Glu Leu Ala Gln Gln Glu Asp Ile Tyr Pro Ala Met
253     610           615           620
255 Pro Glu Pro Ile Arg Lys Cys Pro Gln Cys Asn Lys Asp Met Val Leu
256 625           630           635           640
258 Lys Thr Lys Lys Asn Gly Gly Phe Tyr Leu Ser Cys Met Gly Phe Pro
259         645           650           655
261 Glu Cys Arg Ser Ala Val Trp Leu Pro Asp Ser Val Leu Glu Ala Ser
262         660           665           670
264 Arg Asp Ser Ser Val Cys Pro Val Cys Gln Pro His Pro Val Tyr Arg
265         675           680           685
267 Leu Lys Leu Lys Phe Lys Arg Gly Ser Leu Pro Pro Thr Met Pro Leu
268     690           695           700
270 Glu Phe Val Cys Cys Ile Gly Gly Cys Asp Asp Thr Leu Arg Glu Ile
271 705           710           715           720
273 Leu Asp Leu Arg Phe Ser Gly Gly Pro Pro Arg Ala Ser Gln Pro Ser
274 .         725           730           735
276 Gly Arg Leu Gln Ala Asn Gln Ser Leu Asn Arg Met Asp Asn Ser Gln
277     740           745           750
279 His Pro Gln Pro Ala Asp Ser Arg Gln Thr Gly Ser Ser Lys Ala Leu
280     755           760           765
282 Ala Gln Thr Leu Pro Pro Pro Thr Ala Ala Gly Glu Ser Asn Ser Val
283     770           775           780
285 Thr Cys Asn Cys Gly Gln Glu Ala Val Leu Leu Thr Val Arg Lys Glu
286 785           790           795           800
288 Gly Pro Asn Arg Gly Arg Gln Phe Phe Lys Cys Asn Gly Gly Ser Cys
289         805           810           815
291 Asn Phe Phe Leu Trp Ala Asp Ser Pro Asn Pro Gly Ala Gly Gly Pro
292         820           825           830
294 Pro Ala Leu Ala Tyr Arg Pro Leu Gly Ala Ser Leu Gly Cys Pro Pro
295     835           840           845
297 Gly Pro Gly Ile His Leu Gly Gly Phe Gly Asn Pro Gly Asp Gly Ser
298     850           855           860
300 Gly Ser Gly Thr Ser Cys Leu Cys Ser Gln Pro Ser Val Thr Arg Thr
301 865           870           875           880
303 Val Gln Lys Asp Gly Pro Asn Lys Gly Arg Gln Phe His Thr Cys Ala
304         885           890           895
306 Lys Pro Arg Glu Gln Gln Cys Gly Phe Phe Gln Trp Val Asp Glu Asn
307         900           905           910
309 Thr Ala Pro Gly Thr Ser Gly Ala Pro Ser Trp Thr Gly Asp Arg Gly
310     915           920           925
312 Arg Thr Leu Glu Ser Glu Ala Arg Ser Lys Arg Pro Arg Ala Ser Ser
313     930           935           940
315 Ser Asp Met Gly Ser Thr Ala Lys Lys Pro Arg Lys Cys Ser Leu Cys
316 945           950           955           960
318 His Gln Pro Gly His Thr Arg Pro Phe Cys Pro Gln Asn Arg
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Input Set : A:\st98045sqlt.txt
Output Set: N:\CRF3\10262001\I744125.raw

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323 <212> TYPE: DNA
324 <213> ORGANISM: Homo sapiens
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331 gagcctcaga ttcgtagaat agtcgaacaa gatactatgc ctccaaaggg tgtccgccac   180
333 actatgatgt ttagtgctac ttttcctaag gaaatacaga tgctggctcg tgatttctta   240
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351 gatcttcttg ttgaagctaa acaagaagtg ccgtcttggt tagaaaacat ggcttatgaa   780
353 caccactaca agggtagcag tcgtggacgt tctaagagca gatttagtgg agggtttggt   840
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357 agcagcagcc gcagtggcgg aggtggccac ggtagcagca gaggatttgg tggaggtggc   960
359 tatggaggct tttacaacag tgatggatat ggaggaaatt ataactccca gggggttgac  1020
361 tggtggggta actgagcctg ctttgcagta ggtcaccctg ccaaacaagc taatatggaa  1080
363 accacatgta acttagccag actatacctt gtgtagcttc aagaactcgc agtacattac  1140
365 cagctgtgat tctccactga aatttttttt ttaagggagc tcaaggtcac aagaagaaat  1200
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381             20                  25                  30
383 Asp Arg Met Leu Asp Met Gly Phe Glu Pro Gln Ile Arg Arg Ile Val
384         35                  40                  45
386 Glu Gln Asp Thr Met Pro Pro Lys Gly Val Arg His Thr Met Met Phe
387     50                  55                  60
389 Ser Ala Thr Phe Pro Lys Glu Ile Gln Met Leu Ala Arg Asp Phe Leu
390 65              70                  75                  80
392 Asp Glu Tyr Ile Phe Leu Ala Val Gly Arg Val Gly Ser Thr Ser Glu
393                 85                  90                  95
395 Asn Ile Thr Gln Lys Val Val Trp Val Glu Glu Ser Asp Lys Arg Ser
396             100                 105                 110
398 Phe Leu Leu Asp Leu Leu Asn Ala Thr Gly Lys Asp Ser Leu Thr Leu
399         115                 120                 125
401 Val Phe Val Glu Thr Lys Lys Gly Ala Asp Ser Leu Glu Asp Phe Leu
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